

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 21, 2002, 10:31:33 : Search time 25 Seconds
(without alignments)
793.027 Million cell updates/sec

Title: US-09-943-123-6
Perfect score: 2492
Sequence: 1 MAGVEEVAAGSHLNGDLP.....XHTILLRPTCKEVSRGDDY 478

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2468	99.0	478	1 AMP2_HUMAN	P50579 homo sapien
2	2358	94.6	478	1 AMP2_RAT	P38062 rattus norv
3	2348	94.2	478	1 AMP2_MOUSE	O08663 mus musculu
4	1015	40.7	421	1 AMP2_YEAST	P38174 saccharomyc
5	404	16.2	182	1 YD43_CAEEL	P30581 caenorhabdi
6	393	15.8	295	1 AMPM_PYRFU	P36218 pyrococcus
7	375	15.0	295	1 AMPM_PYRHO	O38362 pyrococcus
8	366	14.7	295	1 AMPM_PYRAB	Q9uvt4 pyrococcus
9	347	13.9	294	1 AMPM_METJA	Q58725 methanococc
10	307	12.3	291	1 AMPM_ARCFU	O28438 archaeoglob
11	295	11.8	299	1 AMPM_METH	O27355 methanobact
12	271.5	10.9	301	1 AMPM_SULSO	P95963 sulfolobus
13	225.5	9.0	394	1 P2G4_HUMAN	Q9uq80 homo sapien
14	225.5	9.0	394	1 P2G4_MOUSE	P50580 mus musculu
15	194.5	7.8	381	1 CBH4_SCHPO	O09184 schizosacch
16	165	6.6	188	1 AMPM_METFE	P22624 methanother
17	145	5.8	712	1 NUCLE_RAT	P13383 rattus norv
18	143	5.7	650	1 NUCLE_XENLA	P20397 xenopus lae
19	140.5	5.6	737	1 PEN_DROME	O61345 drosophila
20	136.5	5.5	1997	1 OTOF_MOUSE	P096f1 mus musculu
21	135.5	5.4	706	1 NUCLE_HUMAN	P19338 homo sapien
22	135	5.4	706	1 NUCLE_MOUSE	P09405 mus musculu
23	135	5.4	1311	1 ATRX_DROME	Q99qns drosophila
24	131	5.3	412	1 FRB4_SPOFR	Q28486 spodoptera
25	128.5	5.2	723	1 SSRP_DROME	Q05344 drosophila
26	126	5.1	767	1 TOP1_CRIGR	Q07050 cricetus
27	124	5.0	1612	1 DNMI_PARLI	Q27746 paracentrot
28	121	4.9	348	1 CYL2_HUMAN	O14093 homo sapien
29	120.5	4.8	845	1 NFM_MOUSE	P12839 rattus norv
30	119.5	4.8	517	1 T2FA_HUMAN	P35269 homo sapien
31	119	4.8	253	1 AMP1_SYNY3	P53579 synechocyst
32	118.5	4.8	542	1 TUL1_HUMAN	O00294 homo sapien
33	118.5	4.8	1359	1 ATRX_CAEEL	Q9u7e0 caenorhabdi

RESULT 1
AMP2_HUMAN
ID AMP2_HUMAN STANDARD; PRT; 478 AA.
AC P50579;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (peptidase M 2)
DE (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).
GN METAP2 OR MNPEP OR P67EIF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95372350; PubMed=7644482;
RA Arfin S.M., Kendall R.B., Hall L., Weaver L.H., Stewart A.E.,
RA Matthews B.W., Bradshaw R.A.;
RT "Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent
enzymes.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95178556; PubMed=7873610;
RA Li X., Chang Y.;
RT "Molecular cloning of a human complementary DNA encoding an
initiation factor 2-associated protein (p67).";
RL Biochim. Biophys. Acta 1260:333-336(1995).
[3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.
RX MEDLINE=99030697; PubMed=9812898;
RA Liu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;
RT "Structure of human methionine aminopeptidase-2 complexed with
fumagillin.";
RL Science 282:1324-1327(1998).
CC -!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
PROTEINS.
CC -!- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
preferentially methionine, from peptides and arylamides.
CC -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC EMBL; U29607; AAA82930.1;
CC EMBL; U13261; AAC63402.1;
CC PDB; 1B59; 14-JAN-00.

P08553 mus musculu
Q61587 mus musculu
P08199 mesocricetu
P46872 stronglyloce
Q99mr6 mus musculu
P46100 homo sapien
Q01662 saccharomyc
Q28181 bos taurus
P91753 lytechinus
Q28092 bos taurus
Q00203 homo sapien
Q08945 homo sapien

ALIGNMENTS

34 118 4.7 848 1 NFM_MOUSE
35 117 4.7 2476 1 ATRX_MOUSE
36 117 4.7 713 1 NUCLE_MOUSE
37 116 4.7 699 1 K122_STRPU
38 115.5 4.6 875 1 ARS2_MOUSE
39 115.5 4.6 2492 1 ATRX_HUMAN
40 115 4.6 387 1 AMP1_YEAST
41 115 4.6 1394 1 CNG4_BOVIN
42 114.5 4.6 411 1 MP62_LYTP1
43 114.5 4.6 488 1 CYL2_BOVIN
44 114.5 4.6 1094 1 A3B1_HUMAN
45 114 4.6 709 1 SSRP_HUMAN

PDB; 1B6A; 11-JAN-00.
DR MEROPS; M24_002; .
DR Genew; HGNC:16672; METAP2.
DR MIM; 601870; .
DR InterPro; IPR002468; MAP_2.
DR InterPro; IPR001714; Methamino_Phase.
DR Pfam; PF00557; Peptidase_M24.
DR PRINTS; PRO0599; MAPEPTIDASE.
DR TIGRFAMs; TIGR00501; met_pdase-II; 1.
DR PROSITE; PS01202; MAP_2; 1.
KW Hydrolase; 360peptide; Cobalt; 3d-structure.
FT DOMAIN 36 46
FT DOMAIN 82 93 ARG/LYS-RICH (BASIC).
FT DOMAIN 98 106 ASP/GLU-RICH (ACIDIC).
FT ACT_SITE 231 231 POLY-LYS.
FT METAL 251 251
FT METAL 262 262 COBALT 2 (BY SIMILARITY).
FT METAL 331 331 COBALT 1 AND 2 (BY SIMILARITY).
FT METAL 331 331 COBALT 1 (BY SIMILARITY).
FT METAL 364 364 COBALT 1 (BY SIMILARITY).
FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
SQ SEQUENCE 478 AA; 52891 MW; 5788E4B83E48F9A CRC64;

Query Match
Best Local Similarity 99.0%; Score 2468; DB 1; Length 478;
Matches 466; Conservative 0; Mismatches 12; Indels 0; Gaps
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DB 1 MAGVEEVAASGSHLNGDLDPDRREGAAGTAEEAAKKRRKKKKSGPSAAGEQEPDKES 60
QY 61 GASVDEVARQLERSALDEKDERDEDDGDDGDDGATGKKKKKKRGPVKVQTDPPSPVI 120
DB 61 GASVDEVARQLERSALDEKDERDEDDGDDGDDGATGKKKKKKRGPVKVQTDPPSPVI 120
QY 121 CDLYPNGVFPKGCECEPYPTQDGRTAARWTTSEBKALDOAEEIWNDFREAAEAHRQVR 180
DB 121 CDLYPNGVFPKGCECEPYPTQDGRTAARWTTSEBKALDOAEEIWNDFREAAEAHRQVR 180
QY 181 KYVSWIKPGMTWIECEKLEDCSRKLIKENGUNAGLAXPTCCSLNNCAAXYTPNAGDTT 240
DB 181 KYVSWIKPGMTWIECEKLEDCSRKLIKENGUNAGLAXPTCCSLNNCAAXYTPNAGDTT 240
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DB 241 VLQYDICKIDFGTHISGRIIDCATVTNPKYDFTLLKAVKDATNTGKICAGIDVRLCDV 300
QY 301 GEAIQEVMSYEVIEDGKTYQVKPIRNXNGXSIGORYXAGTVPYVKGGEATRWEECEV 360
DB 301 GEAIQEVMSYEVIEDGKTYQVKPIRNLNGHSIGORYIHAGCTVPYVKGGEATRWEECEV 360
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DB 361 YALITFGSTGKGVVHDDMECSHYMKNFVDGVHPRLPRTKHLNINVENFGTLAFCRRWL 420
QY 421 DRLGESKYLMAKLNCLDLGIVDPXPPXCOIKGVSYTAOFXHTILLRPTCKEVVSRGDDY 478
DB 421 DRLGESKYLMAKLNCLDLGIVDPYPLCDIKGVSYTAOFHTILLRPTCKEVVSRGDDY 478

RESULT 2
AMP2_RAT
ID AMP2_RAT STANDARD; PRT; 478 AA.
AC P38062;
DT 01-OCT-1994 (Rel. 30, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
ID 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
GN (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eif2).
OR METAP2 OR MNPEP OR P67EIF2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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/translation="MAGVEEVAAGSHLNGLDLPDDR EGAASTAEAAKKRRRKKK
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BASE COUNT							
ORIGIN							
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Query Match	99.7%	Score	1432.8	DB	9	Length	2569
Best Local Similarity	99.8%	Pred. No.	0				
Mismatches	1434	Conservative	0	Mismatches	3	Indels	0
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61	GACGACAGGAGACAGGAGCTGCCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGACGA	120					
83	GACGACAGGAGACAGGAGCTGCCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGACGA	142					
121	AGCAAGAGAGAGACAGGAGCTGCCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGACGA	180					
143	AGCAAGAGAGAGACAGGAGCTGCCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGACGA	202					
181	GGAGCCCTCAGTGGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	240					
203	GGAGCCCTCAGTGGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	262					
241	AGAGATGAAGATGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	300					
263	AGAGATGAAGATGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	322					
301	AAAAAG	360					
323	AAAAAG	382					
361	TGTGACCTGTATCTTAATGTGTATTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420					
383	TGTGACCTGTATCTTAATGTGTATTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	442					
421	CAAGATGGCGCAACAGCTGCTTGAGAACTACAAAGTGAAGAAAGAGAGAGAGAGAGAG	480					
443	CAAGATGGCGCAACAGCTGCTTGAGAACTACAAAGTGAAGAAAGAGAGAGAGAGAGAG	502					
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503	GCAAGTGAAGAGATTGGAATGATTTTCGAGAAGCTGAGAGAGAGAGAGAGAGAGAGAG	600					
541	AAATACGTAATGAGCTGATCAAGCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGG	622					
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683	ACTGGATGTTCTCTCAATANTGCTGCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGG	742					
721	GTATTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	780					
743	GTATTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	802					
781	ATTGACTGCTGCTTTTACTGTCACCTTTTAAATCCCAATATGATGATGATGATGATGATGAT	840					
803	ATTGACTGCTGCTTTTACTGTCACCTTTTAAATCCCAATATGATGATGATGATGATGATGAT	862					
841	AAAGATGCTACTAAACACTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	900					
863	AAAGATGCTACTAAACACTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	922					

901	GGTGGAGCCATCCAAAGATTATGAGTCTCTATGAAGTTGAAATAGATGGGAGACATAT	960
923	GGTGGAGCCATCCAAAGATTATGAGTCTCTATGAAGTTGAAATAGATGGGAGACATAT	982
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1043	GGAAAAACAGTGGCGGATTTGTAAGAGGAGGAGGCAACAAAGATGGAGGAGGAGAGTA	1102
1081	TATGCAATTTGAACCTTTTGGTAGTACAGGAAAAAGGTGTTGTTGATGATGATGATGATGAT	1140
1103	TATGCAATTTGAACCTTTTGGTAGTACAGGAAAAAGGTGTTGTTGATGATGATGATGATGAT	1162
1141	TCACATTACATGAAAAATTTTTCATGTTGACATGTTGCCAATAGGCTTCCCAAGAACAAA	1200
1163	TCACATTACATGAAAAATTTTTCATGTTGACATGTTGCCAATAGGCTTCCCAAGAACAAA	1222
1201	CACCTTTAAATGTCATCAATGAAACCTTTTGAACCTTTTGAACCTTTTGAACCTTTTGA	1260
1223	CACCTTTAAATGTCATCAATGAAACCTTTTGAACCTTTTGAACCTTTTGAACCTTTTGA	1282
1261	GATCGCTTGGGAGAGAGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT	1320
1283	GATCGCTTGGGAGAGAGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT	1342
1321	GTACATCCATATCCACCATTTATGATGATGATGATGATGATGATGATGATGATGATGAT	1380
1343	GTACATCCATATCCACCATTTATGATGATGATGATGATGATGATGATGATGATGATGAT	1402
1381	ACCATCTCTGTTGGTCCCAACATGTAAGAGATTTGTCAGCAGAGGAGATGACTATTA	1437
1403	ACCATCTCTGTTGGTCCCAACATGTAAGAGATTTGTCAGCAGAGGAGATGACTATTA	1459
RESULT 3		
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LOCUS	G28539	DNA linear STS 11-JUL-1996
DEFINITION	G28539	
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KEYWORDS	Homo sapiens	
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 2569)	
AUTHORS	Myers,R.M.	
JOURNAL	Unpublished (1996)	
COMMENT	Contact: Richard M. Myers Stanford Human Genome Center (SHGC) Stanford University School of Medicine Department of Genetics, M-344, Stanford, CA 94305, USA Tel: 415/7259687 Fax: 415/7259689 Email: myers@shgc.stanford.edu	
Primer A: CAAAGCCACCTCAACACCTT		
Primer B: AGGAGGGGAAAAACAGTAGC		
STS size: 216		
PCR Profile:		
Initial incubation: 94 degrees C for 90 seconds		
Denaturation: 94 degrees C for 15 seconds		
Annealing: 62 degrees C for 23 seconds		
Polymerization: 72 degrees C for 30 seconds		
PCR Cycles: 30		
Thermal Cycler: Perkin Elmer 9600		
Protocol:		

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 21, 2002, 10:31:33 ; Search time 25 Seconds
(without alignments)
793.027 Million cell updates/sec

Title: US-09-943-123-6
Perfect score: 2492
Sequence: 1 MAGVEEVAASGSHLNGDLP.....XHTLLRPTCKEVVSRGGDY 478

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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9	347	13.9	294	1 AMPM_METJA	O28438 archaeoglob
10	307	12.3	291	1 AMPM_ARCFU	O27355 methanobact
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14	225.5	9.0	394	1 P2G4_MOUSE	O09184 schizosacch
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18	143	5.7	650	1 NUCLE_XENLA	O61345 drosophila
19	140.5	5.6	737	1 PEN_DROME	O9est1 mus musculu
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21	135.5	5.4	706	1 NUCLE_HUMAN	P09405 mus musculu
22	135	5.4	706	1 NUCLE_MOUSE	O9eqn5 drosophila
23	135	5.4	1311	1 ATRX_DROME	O26486 spodoptera
24	131	5.3	412	1 FKBA_SPOFR	O05344 drosophila
25	128.5	5.2	723	1 SSRP_DROME	O07050 cricetus
26	126	5.1	767	1 TOP1_CRIGR	O27746 paracentrot
27	124	5.0	1612	1 DNML_PARLI	Q14093 homo sapien
28	121	4.9	348	1 CYL2_HUMAN	P12839 rattus norv
29	120.5	4.8	845	1 NFM_RAT	P35269 homo sapien
30	119.5	4.8	517	1 T2FA_HUMAN	P53579 synechocyst
31	119	4.8	253	1 AMPL_SYNY3	O00294 homo sapien
32	118.5	4.8	542	1 TULL_HUMAN	O9u7e0 caenorhabdi
33	118.5	4.8	1359	1 ATRX_CAEEL	

34	118	4.7	848	1 NFM_MOUSE	P08553 mus musculu
35	118	4.7	2476	1 ATRX_MOUSE	Q01687 mus musculu
36	117	4.7	713	1 NUCLE_MESAU	P08199 mesocricetu
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39	115.5	4.6	2492	1 ATRX_HUMAN	P46100 homo sapien
40	115	4.6	387	1 AMP1_YEAST	Q01662 saccharomyc
41	115	4.6	1394	1 CNG4_BOVIN	Q28181 bos taurus
42	114.5	4.6	411	1 MP62_LYTP1	P91753 lytechinus
43	114.5	4.6	488	1 CYL2_BOVIN	Q28092 bos taurus
44	114.5	4.6	1094	1 A3B1_HUMAN	O00203 homo sapien
45	114	4.6	709	1 SSRP_HUMAN	Q08943 homo sapien

ALIGNMENTS

ID	AMP2_HUMAN	STANDARD	PRT	478 AA
AC	P50579			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)			
DE	(Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).			
GN	METAP2 OR MNPEP OR p67EIF2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	MEDLINE=95372350; PubMed=7644482;			
RA	Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,			
RA	Matthews B.W., Bradshaw R.A.;			
RT	"Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent enzymes";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	MEDLINE=95178556; PubMed=7873610;			
RA	Li X., Chang Y.;			
RT	"Molecular cloning of a human complementary DNA encoding an initiation factor 2-associated protein (p67).";			
RL	Biochim. Biophys. Acta 1260:333-336(1995).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.			
RA	MEDLINE=99030697; PubMed=9812898;			
RA	Liu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;			
RT	"Structure of human methionine aminopeptidase-2 complexed with fumagillin.";			
RL	Science 282:1324-1327(1998).			
CC	- - FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS.			
CC	- - CATALYTIC ACTIVITY: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides.			
CC	- - COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).			
CC	- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.			
CC	-----			
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CC	-----			
CC	EMBL; U29607; AAA82930.1; -			
DR	EMBL; U13261; AAC63402.1; -			
DR	PDB; 1B59; 14-JAN-00.			

DR PDB: 1B6A; 11-JAN-00.
 DR MEROPS; M24.002; .
 DR Genew; HGNC:16672; METAP2.
 DR MIM; 601870; .
 DR InterPro; IPR002468; MAP_2.
 DR InterPro; IPR001714; Methamino_Ptase.
 DR InterPro; IPR000994; Peptidase_M24.
 DR Pfam; PF00557; Peptidase_M24; 1.
 DR PRINTS; PR00599; MAPEPTIDASE.
 DR TIGRFAMs; TIGR00501; met_pdase-II; 1.
 DR PROSITE; PS01202; MAP_2; 1.
 DR Hydrolase; AminoPeptidase; Cobalt; 3D-structure.
 FT DOMAIN 36 46 ARG/LYS-RICH (BASIC).
 FT DOMAIN 82 93 ASP/GLU-RICH (ACIDIC).
 FT ACT_SITE 231 231 POLY-LYS.
 FT METAL 251 251 COBALT 2 (BY SIMILARITY).
 FT METAL 262 262 COBALT 1 AND 2 (BY SIMILARITY).
 FT METAL 331 331 COBALT 1 (BY SIMILARITY).
 FT METAL 364 364 COBALT 1 (BY SIMILARITY).
 FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
 SQ SEQUENCE 478 AA; 52891 MW; 5788E4B83E48F9A CRC64;

Query Match 99.0%; Score 2468; DB 1; Length 478;
 Best Local Similarity 97.5%; Pred. No. 1e-154;
 Matches 466; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAGVEEVAASGSHLNDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60
 DB 1 MAGVEEVAASGSHLNDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60

QY 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKRRKKKRRKGRPKVQTDPPSVPI 120
 DB 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKRRKKKRRKGRPKVQTDPPSVPI 120

QY 121 CDLYPNGVFPKQCEYPTPDGRTAAWRTTSEKKALDOASEEINWDPREAAEAHQVR 180
 DB 121 CDLYPNGVFPKQCEYPTPDGRTAAWRTTSEKKALDOASEEINWDPREAAEAHQVR 180

QY 181 KYVMSWIKPGMTMIEICEKLEDCSKLTKENGLNAGLAXPTGCSLNCAAXYTPNAGDTT 240
 DB 181 KYVMSWIKPGMTMIEICEKLEDCSKLTKENGLNAGLAFPTGCSLNCAAHYTPNAGDTT 240

QY 241 VLQYDDICKIXFGTHISGRITXCAFTVTFNPKYDTLLKAVDAWNTGKICAGIDVRLCDV 300
 DB 241 VLQYDDICKIDFGTHISGRITDCAFTVTFNPKYDTLLKAVDAWNTGKICAGIDVRLCDV 300

QY 301 GEATQEVNYESVEIDGKTYQVKPIRNKXGXSIGQYRXAGKTYPIVKGGEATRMEEGEV 360
 DB 301 GEATQEVNYESVEIDGKTYQVKPIRNKXGXSIGQYRIHAGKTYPIVKGGEATRMEEGEV 360

QY 361 YAIITFGSTGKGVVDDMECSHYMKNFVDGHPVIRLPRTKHLLNVIENFGTLAFRCRWL 420
 DB 361 YAIITFGSTGKGVVDDMECSHYMKNFVDGHPVIRLPRTKHLLNVIENFGTLAFRCRWL 420

QY 421 DRLGESKYLKALNCLDGLVDPXPPXCDITKGSVTAQFXTILLRPTCKEVSRGDDY 478
 DB 421 DRLGESKYLKALNCLDGLVDPXPPXCDITKGSVTAQFXTILLRPTCKEVSRGDDY 478

RESULT 2
 AMP2_RAT ID AMP2_RAT STANDARD; PRT; 478 AA.
 AC P38062;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
 GN (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Reuber H35; TISSUE=Liver;
 RX MEDLINE=93266517; PubMed=8496145;
 RA Wu S., Gupta S., Chatterjee N., Hileman R.E., Kinzy T.G.,
 RA Denslow N.D., Merrick W.C., Chakrabarti D., Osterman J.C., Gupta N.K.;
 RT "Cloning and characterization of complementary DNA encoding the
 RT eukaryotic initiation factor 2-associated 67-kDa protein (p67).";
 RL J. Biol. Chem. 268:10796-10801(1993).
 RN [2]
 RP REVISIONS TO C-TERMINUS
 RX MEDLINE=95372350; PubMed=7644482;
 RA Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,
 RA Matthews B.W., Bradshaw R.A.;
 RT "Eukaryotic methionyl aminopeptidases: two classes of
 RT cobalt-dependent enzymes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
 CC -1- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
 CC PROTEINS.
 CC -1- PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE
 CC REGULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE
 CC EIF-2 GAMMA-SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
 CC preferentially methionine, from peptides and arylamides.
 CC -1- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (BY SIMILARITY).
 CC -1- PTM: CONTAINS 12 O-LINKED GLCNAC.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.
 CC
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 CC or send an email to license@isb-sib.ch.
 CC
 CC EMBL; LI0652; AAA41111.1;
 CC PIR; A46702; A46702.
 CC HSSP; P50579; 1B6A.
 CC MEROPS; M24.002; .
 CC InterPro; IPR002468; MAP_2.
 CC InterPro; IPR001714; Methamino_Ptase.
 CC InterPro; IPR000994; Peptidase_M24.
 CC Pfam; PF00557; Peptidase_M24; 1.
 CC PRINTS; PR00599; MAPEPTIDASE.
 CC TIGRFAMs; TIGR00501; met_pdase-II; 1.
 CC PROSITE; PS01202; MAP_2; 1.
 CC Hydrolase; AminoPeptidase; Cobalt; Glycoprotein.
 FT DOMAIN 36 46 ARG/LYS-RICH (BASIC).
 FT DOMAIN 82 93 ASP/GLU-RICH (ACIDIC).
 FT METAL 251 251 COBALT 2 (BY SIMILARITY).
 FT METAL 262 262 COBALT 1 AND 2 (BY SIMILARITY).
 FT METAL 331 331 COBALT 1 (BY SIMILARITY).
 FT METAL 364 364 COBALT 1 (BY SIMILARITY).
 FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
 FT CONFLICT 464 478 LPTCKEVSRGDDY -> CAQPVKKLSAEWTKT (IN
 FT REF. 1).
 SQ SEQUENCE 478 AA; 53052 MW; BEIC0E91EOCB3D74 CRC64;

Query Match 94.6%; Score 2358; DB 1; Length 478;
 Best Local Similarity 92.5%; Pred. No. 1.6e-147;
 Matches 442; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 MAGVEEVAASGSHLNDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60
 DB 1 MAGVEEVAASGSHLNDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60

QY 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKRRKKKRRKGRPKVQTDPPSVPI 120
 DB 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKRRKKKRRKGRPKVQTDPPSVPI 120

KKKRGPKVOTDPPSPVPCIDLYPNVFPKQCEYPTDQRTAAWRTTSEEKALDQ
ASEIWNDFREAAEHROVKRYWMIKPMWMIIEICEKLEDSCSRKLIKENGINAGLA
FPTGCSLNNCAHYTNPAGDTVLQYDDICKIDFTHISGRIDCAFTVFNPKYDPL
LKAVDANTNIGKACGIDVRLDGEAIOEVMESYEVEIDGKTYQVAPIRNLNGSHG
QYRHAGKTVPYIKVGGGATRMEBEVEVAIETFGSTGKGVVHDDMECSHYMKNFYCDI
PIRLPRTKHLNINENFENFTLAFRCRWLDRLESKYLMLKLNLDLGIYDVPPLCDI
KGSYTAQFEHTILLRPTCKEVVSRGDDT*
BASE COUNT 957 a 468 c 542 g 602 t

ORIGIN	Query Match	Score	1432.8;	DB 9;	Length	2569;
	Best Local Similarity	99.7%;				
	Matches 1434; Conservative	99.8%;				
		0; Mismatches	3;	Indels	0;	Gaps
QY	1	ATGCGGGCGGTGAGGAGGTAGCGGCTCCGGGAGGACCCCTGAATGCGGACCTGGATCCA	60			
DB	23	ATGCGGGCGGTGAGGAGGTAGCGGCTCCGGGAGGACCCCTGAATGCGGACCTGGATCCA	82			
QY	61	GACGACAGGAGNAGAGAGGTGCTCTACGCGTGAAGAGCAGCAAGAAAAAGACGA	120			
QY	83	GACGACAGGAGNAGAGAGGTGCTCTACGCGTGAAGAGCAGCAAGAAAAAGACGA	142			
DB	121	AAGAGAGAGAGAGCAAGAGGCGCTTCTGACGAGGAGCAAGCAAGCACTGATAAGATCA	180			
QY	143	AAGAGAGAGAGAGCAAGAGGCGCTTCTGACGAGGAGCAAGCAAGCACTGATAAGATCA	202			
DB	181	GGAGCCTCAGTGGATGAGTACGACAGTGTGGAAGATGACGATGGAAGTAAAGAA	240			
QY	203	GGAGCCTCAGTGGATGAGTACGACAGTGTGGAAGATGACGATGGAAGTAAAGAA	262			
DB	241	AGAGATGAAGATGATGAGATGAGATGCGGATGGAGATGGAGCACTGGAAGAGAG	300			
QY	263	AGAGATGAAGATGATGAGATGAGATGCGGATGGAGATGGAGCACTGGAAGAGAG	322			
DB	301	AAAAAGAGAGAGAGAGAGAGGAGGACCAAGATTTCAACAGACCCCTCCCTCAGTTCCA	360			
QY	323	AAAAAGAGAGAGAGAGAGAGGAGGACCAAGATTTCAACAGACCCCTCCCTCAGTTCCA	382			
DB	361	TGTGACCTGTATCTTATGTTGTTATTTCCCAAGGACCAAGATGCGGATGCGGATGCGG	420			
QY	383	TGTGACCTGTATCTTATGTTGTTATTTCCCAAGGACCAAGATGCGGATGCGGATGCGG	442			
DB	421	CAAGATGCGGAGAGAGTGTGTTGAGAACTACAACTGAAGAGAGAGAGAGAGAGAGAG	480			
QY	443	CAAGATGCGGAGAGAGTGTGTTGAGAACTACAACTGAAGAGAGAGAGAGAGAGAGAG	502			
DB	481	GCAAGTGAAGAGATTTGGATGATTTTCGAGAGAGTTCGAGAGAGAGAGAGAGAGAG	540			
QY	503	GCAAGTGAAGAGATTTGGATGATTTTCGAGAGAGTTCGAGAGAGAGAGAGAGAGAG	562			
DB	541	AAATAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600			
QY	563	AAATAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	622			
DB	601	GAGAGCTGTTCAACCAAGTAAATAAGAGAGATGATGATGATGATGATGATGATGATGAT	660			
QY	623	GAGAGCTGTTCAACCAAGTAAATAAGAGAGATGATGATGATGATGATGATGATGATGAT	682			
DB	661	ACTGATGTTCTCTCAATAATTTGCTGCGCCNTATCTCCCAATGCGCGGTGACACA	720			
QY	683	ACTGATGTTCTCTCAATAATTTGCTGCGCCNTATCTCCCAATGCGCGGTGACACA	742			
DB	721	GTATTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780			
QY	743	GTATTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	802			
DB	781	ATTGACTGTCTTTTACTGTCACTTTTAAATGAGAGATGATGATGATGATGATGATGAT	840			
QY	803	ATTGACTGTCTTTTACTGTCACTTTTAAATGAGAGATGATGATGATGATGATGATGAT	862			
DB	841	AAAGATGCTACTACACTGGAATAAGTGTGCTGGAATTTGATGTTCTGCTGTGATGTT	900			
QY	863	AAAGATGCTACTACACTGGAATAAGTGTGCTGGAATTTGATGTTCTGCTGTGATGTT	922			

QY	901	GGTGAGGCGCATCCAAAGAGTTTATGAGTCCCTATGAAGTTGAATAGATGGGAAGACATAT	960
DB	923	GGTGAGGCGCATCCAAAGAGTTTATGAGTCCCTATGAAGTTGAATAGATGGGAAGACATAT	982
QY	961	CAAGTGAARACCAATCCGTAATCTAAATGACATCTCAATTTGGCAATATAGAAATACATGCT	1020
DB	983	CAAGTGAARACCAATCCGTAATCTAAATGACATCTCAATTTGGCAATATAGAAATACATGCT	1042
QY	1021	GGAAAAACAGTCCGATTTGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1080
DB	1043	GGAAAAACAGTCCGATTTGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1102
QY	1081	TATGCAATTTGAAACCTTTGTTGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140
DB	1103	TATGCAATTTGAAACCTTTGTTGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1162
QY	1141	TCACATTTACATGAAAAATTTTGTGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1200
DB	1163	TCACATTTACATGAAAAATTTTGTGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1222
QY	1201	CACCTTTTAAATGTCATCAATGAAACCTTTGGAACCTTTGGAACCTTTGGAACCTTTGGA	1260
DB	1223	CACCTTTTAAATGTCATCAATGAAACCTTTGGAACCTTTGGAACCTTTGGAACCTTTGGA	1282
QY	1261	GATCGCTTTGGGAGAGTAAATGTTGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1320
DB	1283	GATCGCTTTGGGAGAGTAAATGTTGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1342
QY	1321	GTAGATCCATATCCACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT	1380
DB	1343	GTAGATCCATATCCACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT	1402
QY	1381	ACCATCTCTGTTGCTCCCAACATGTAAGAGAGTGTGTAAGAGAGTGTGTAAGAGAGTGT	1437
DB	1403	ACCATCTCTGTTGCTCCCAACATGTAAGAGAGTGTGTAAGAGAGTGTGTAAGAGAGTGT	1459

RESULT 3
LOCUS G28539 human STS SHGC-31600, sequence tagged site.
DEFINITION G28539
ACCESSION G28539.1 GI:1408354
VERSION STS; STS sequence; primer; sequence tagged site.
KEYWORDS Homo sapiens.
SOURCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2569)
AUTHORS Myers, R.W.
JOURNAL Unpublished (1996)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CAAAGCCACCTCAACACCTT
Primer B: AGGAAGGGGAAAAACAGTTAGC
STS size: 216
PCR profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol: